

SEQUENCE LISTING

<110> Gao, Zeren
Hart, Charles E.
Piddington, Christopher S.
Sheppard, Paul O.
Shoemaker, Kimberly E.
Gilbertson, Debra G.
West, James W.

<120> GROWTH FACTOR HOMOLOG ZVEGF3

<130> 98-60

<160> 50

<170> FastSEQ for Windows Version 3.0

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<211> 1760

<212> DNA

<213> Homo sapiens

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<221> CDS

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cgccgtgagt gagctctcac ccagtcagc caa atg agc ctc ttc ggg ctt ctc	174
Met Ser Leu Phe Gly Leu Leu	
1 5	
ctg ctg aca tct gcc ctg gcc ggc cag aga cag ggg act cag gcg gaa	222
Leu Leu Thr Ser Ala Leu Ala Gly Gln Arg Gln Gly Thr Gln Ala Glu	
10 15 20	
tcc aac ctg agt agt aaa ttc cag ttt tcc agc aac aag gaa cag aac	270
Ser Asn Leu Ser Ser Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn	
25 30 35	

gga gta caa gat cct cag cat gag aga att att act gtg tct act aat	318
Gly Val Gln Asp Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn	
40 45 50 55	
gga agt att cac agc cca agg ttt cct cat act tat cca aga aat acg	366
Gly Ser Ile His Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn Thr	
60 65 70	
gtc ttg gta tgg aga tta gta gca gta gag gaa aat gta tgg ata caa	414
Val Leu Val Trp Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln	
75 80 85	
ctt acg ttt gat gaa aga ttt ggg ctt gaa gac cca gaa gat gac ata	462
Leu Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile	
90 95 100	
tgc aag tat gat ttt gta gaa gtt gag gaa ccc agt gat gga act ata	510
Cys Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Thr Ile	
105 110 115	
tta ggg cgc tgg tgt ggt tct ggt act gta cca gga aaa cag att tct	558
Leu Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser	
120 125 130 135	
aaa gga aat caa att agg ata aga ttt gta tct gat gaa tat ttt cct	606
Lys Gly Asn Gln Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro	
140 145 150	
tct gaa cca ggg ttc tgc atc cac tac aac att gtc atg cca caa ttc	654
Ser Glu Pro Gly Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe	
155 160 165	
aca gaa gct gtg agt cct tca gtg cta ccc cct tca gct ttg cca ctg	702
Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu	
170 175 180	
gac ctg ctt aat aat gct ata act gcc ttt agt acc ttg gaa gac ctt	750
Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu	
185 190 195	
att cga tat ctt gaa cca gag aga tgg cag ttg gac tta gaa gat cta	798
Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu	
200 205 210 215	

141

55222 9923456

tat agg cca act tgg caa ctt ctt ggc aag gct ttt gtt ttt gga aga 846
 Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys/Ala Phe Val Phe Gly Arg
 220 225 230

aaa tcc aga gtg gtg gat ctg aac ctt cta aca gag gag gta aga tta 894
 Lys Ser Arg Val Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu
 235 240 245

tac agc tgc aca cct cgt aac ttc tca gtg tcc ata agg gaa gaa cta 942
 Tyr Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu
 250 255 260

aag aga acc gat acc att ttc tgg cca ggt tgt ctc ctg gtt aaa cgc 990
 Lys Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg
 265 270 275

tgt ggt ggg aac tgt gcc tgt tgt ctc cac aat tgc aat gaa tgt caa 1038
 Cys Gly Gly Asn Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln
 280 285 290 295

tgt gtc cca agc aaa gtt act aaa aaa tac cac gag gtc ctt cag ttg 1086
 Cys Val Pro Ser Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu
 300 305 310

aga cca aag acc ggt gtc agg gga ttg cac aaa tca ctc acc gac gtg 1134
 Arg Pro Lys Thr Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val
 315 320 325

gcc ctg gag cac cat gag gag tgt gac tgt gtg tgc aga ggg agc aca 1182
 Ala Leu Glu His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr
 330 335 340

gga gga tag ccgcatcacc accagcagct cttgcccaga gctgtgcagt 1231
 Gly Gly *
 345

gcagtggctg attctattag agaacgtatg cgttatctcc atccttaatc tcagttgttt 1291
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142

5' to 3' direction

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 <213> Homo sapiens

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Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe	Gln	Phe
			20					25					30		
Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	His	Glu	Arg
		35					40					45			
Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	Pro	Arg	Phe	Pro
	50					55					60				
His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	Arg	Leu	Val	Ala	Val
65					70					75					80
Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	Asp	Glu	Arg	Phe	Gly	Leu
			85						90					95	
Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	Tyr	Asp	Phe	Val	Glu	Val	Glu
			100					105					110		
Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr
		115					120					125			
Val	Pro	Gly	Lys	Gln	Ile	Ser	Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe
	130					135					140				
Val	Ser	Asp	Glu	Tyr	Phe	Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr
145					150					155					160
Asn	Ile	Val	Met	Pro	Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu
			165						170					175	
Pro	Pro	Ser	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala
			180					185						190	
Phe	Ser	Thr	Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp
		195					200					205			
Gln	Leu	Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly
	210					215					220				
Lys	Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu
225					230					235					240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	Ser
			245						250					255	
Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	Trp	Pro
			260					265					270		
Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	Cys	Cys	Leu
		275					280					285			
His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	Val	Thr	Lys	Lys
	290					295					300				

143

654321 " 99045460

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
305 310 315 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
325 330 335
Cys Val Cys Arg Gly Ser Thr Gly Gly
340 345

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<223> Xaa is any amino acid
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<223> Xaa is any amino acid or not present
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144

<223> Xaa is any amino acid not present

<221> VARIANT

<222> (115)...(115)

<223> Xaa is any amino acid

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Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Cys	Xaa	Gly	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		35					40						45		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		50				55					60				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65						70				75					80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105						110	
Xaa	Cys	Xaa	Cys												
			115												

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<223> peptide motif

<221> VARIANT

<222> (2)...(2)

<223> Xaa is Lys or Arg

<221> VARIANT

<222> (4)...(4)

<223> Xaa is Asp, Asn or Glu

<221> VARIANT

<222> (5)...(5)

<223> Xaa is Trp, Tyr or Phe

<221> VARIANT

145

<222> (6)...(16)

<223> Xaa is any amino acid

<221> VARIANT

<222> (17)...(20)

<223> Xaa is any amino acid or not present

<221> VARIANT

<222> (22)...(22)

<223> Xaa is Lys or Arg

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<222> (23)...(23)

<223> Xaa is Trp, Tyr or Phe

<400> 4

Cys	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10						15		
Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Cys									
				20												

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<223> peptide tag

<400> 5

Glu	Tyr	Met	Pro	Met	Glu
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<210> 6

<211> 1035

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<223> degenerate sequence derived from SEQ ID NOS: 1 and 2

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<223> n = A,T,C or G

146

652021" 99025450

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gtncargay	c	ncarcay	ga	rmgnathath	acngtnwsna	cnaaygg	180
ccnmgn	tt	yc	ncayacnta	yccnmgnaay	acngtnytn	g	240
gargaraay	g	tntggath	ca	rytnacnt	ty	gaygarmgnt	300
gaygayat	h	g	yaartayga	y	tt	ygtn	360
ggnmgn	t	g	g	ggnwsng	g	nacngtnccn	420
mg	nath	m	gnt	ty	gtnwsnga	y	480
aayath	g	t	na	tgccncart	t	yacngargcn	540
ytnccny	t	g	n	ayytnytn	aa	yaaygc	600
mgntay	y	t	g	n	arccngarm	g	660
carytny	t	g	n	gnaargc	nt	ygtnttygg	720
ytnacng	arg	tn	m	gny	nt	aywsntgy	780
gargary	tna	arm	gnacng	a	yacnath	tt	840
ggnggna	ay	t	gygc	ntgyt	g	yytn	900
gtnacna	ara	artay	cayga	rgtnytn	car	ytnmg	960
cayaar	wsny	tnacng	aygt	ngcnytn	gar	caycayg	1020
ggnwsna	cng	gnggn					1035

<210> 7

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> n = A,T,C or G

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mgntgyggng gnaaytg

17

<210> 8

<211> 17

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<221> misc_feature

147

<222> (1)...(17)

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mgntgydsng gnwrytg

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<210> 9

<211> 17

<212> DNA

<213> Artificial Sequence

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<222> (1)...(17)

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<400> 9

carywnccns hrcanck

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ttytggccng gntggyt

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<210> 11

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer

<221> misc_feature

148

<222> (1)...(17)

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ntnddnccnn sntgybt

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<210> 12

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avrcansng gnhhnan

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<210> 13

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 13

caygargart gygaytg

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<210> 14

<211> 17

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<400> 14

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<210> 19
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<400> 19
 tgyaartayg aytwygt

17

<210> 20
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<400> 20
 acrwartcrt ayttrca

17

<210> 21
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151

<223> Oligonucleotide primer

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ywnngnmrnt dbtgygg

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<210> 22

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<222> (1)...(17)

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ccrcavhany knccnwr

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<400> 23

tdbccnmand vntaycc

17

<210> 24

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152

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<221> misc_feature

<222> (1)...(17)

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ggrtanbhnt knggyha

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agcaggtcca gtggcaaagc

20

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<212> DNA

<213> Artificial Sequence

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cgtttgatga aagatttggg c

21

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer

<400> 27

ggaggtctat ataagcagag c

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tctggacgtc ctctgctgg tatag

25

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 31

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<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

652621 332563

154

<220>

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27

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<400> 33

cttttgctag cctcaaccct gactatc

27

<210> 34

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC20,180

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cgcgcggttt aaacgccacc atgagcctct tcggg

35

<210> 35

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC20,181

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cgtatcggcg cgccctatcc tcctgtgctc cc

32

<210> 36

<211> 1882

<212> DNA

<213> Homo sapiens

155

<220>

<221> CDS

<222> (226)...(1338)

<400> 36

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cagggcgagc gcaggcggcg agagcgagg gcggcgcggtc gtcggtcccg ggagcagaac
ccggcttttt cttggagcga cgctgtctct agtcgctgat ccaa atg cac cgg ctc
Met His Arg Leu

```

1

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atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc tgt cgg gac
Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser Cys Arg Asp
5 10 15 20

```

```

act tct gca acc ccg cag agc gca tcc atc aaa gct ttg cgc aac gcc
Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu Arg Asn Ala
25 30 35

```

```

aac ctc agg cga gat gag agc aat cac ctc aca gac ttg tac cga aga
Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu Tyr Arg Arg
40 45 50

```

```

gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag agt cct aga
Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln Ser Pro Arg
55 60 65

```

```

ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg cgg ctt cac
Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Arg Leu His
70 75 80

```

```

tct cag gag aat aca cgg ata cag cta gtg ttt gac aat cag ttt gga
Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn Gln Phe Gly
85 90 95 100

```

```

tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt gtg gaa gtt
Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val
105 110 115

```

```

gaa gat ata tcc gaa acc agt acc att att aga gga cga tgg tgt gga
Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg Trp Cys Gly
120 125 130

```

156

cac aag gaa gtt cct cca agg ata aaa tca aga acg aac caa att aaa	669
His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn Gln Ile Lys	
135 140 145	
atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct gga ttc aag	717
Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys	
150 155 160	
att tat tat tct ttg ctg gaa gat ttc caa ccc gca gca gct tca gag	765
Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala Ala Ala Ser Glu	
165 170 175 180	
acc aac tgg gaa tct gtc aca agc tct att tca ggg gta tcc tat aac	813
Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly Val Ser Tyr Asn	
185 190 195	
tct cca tca gta acg gat ccc act ctg att gcg gat gct ctg gac aaa	861
Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp Ala Leu Asp Lys	
200 205 210	
aaa att gca gaa ttt gat aca gtg gaa gat ctg ctc aag tac ttc aat	909
Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn	
215 220 225	
cca gag tca tgg caa gaa gat ctt gag aat atg tat ctg gac acc cct	957
Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro	
230 235 240	
cgg tat cga ggc agg tca tac cat gac cgg aag tca aaa gtt gac ctg	1005
Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser Lys Val Asp Leu	
245 250 255 260	
gat agg ctc aat gat gat gcc aag cgt tac agt tgc act ccc agg aat	1053
Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn	
265 270 275	
tac tcg gtc aat ata aga gaa gag ctg aag ttg gcc aat gtg gtc ttc	1101
Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala Asn Val Val Phe	
280 285 290	
ttt cca cgt tgc ctc ctc gtg cag cgc tgt gga gga aat tgt ggc tgt	1149
Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly Asn Cys Gly Cys	
295 300 305	

157

gga act gtc aac tgg agg tcc tgc aca tgc aat tca ggg aaa acc gtg 1197
 Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser Gly Lys Thr Val
 310 315 320

aaa aag tat cat gag gta tta cag ttt gag cct ggc cac atc aag agg 1245
 Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly His Ile Lys Arg
 325 330 335 340

agg ggt aga gct aag acc atg gct cta gtt gac atc cag ttg gat cac 1293
 Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile Gln Leu Asp His
 345 350 355

cat gaa cga tgc gat tgt atc tgc agc tca aga cca cct cga taa 1338
 His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro Pro Arg *
 360 365 370

gagaatgtgc acatccttac attaagcctg aaagaacctt tagtttaagg aggggtgagat 1398
 aagagaccct tttcctacca gcaaccaaac ttactactag cctgcaatgc aatgaacaca 1458
 agtggttgct gagtctcagc cttgctttgt taatgccatg gcaagtagaa aggtatatca 1518
 tcaacttcta tacctaagaa tataggattg catttaataa tagtgtttga gggtatatat 1578
 gcacaaacac acacagaaat atattcatgt ctatgtgtat atagatcaaa tgtttttttt 1638
 ttttggtata tataaccagg tacaccagag gttacatatg tttgagttag actcttaaaa 1698
 tcctttgccaa aaataaggga tgggtcaaata tatgaaacat gtcttttagaa aatttaggag 1758
 ataaatttat ttttaaattt tgaaacacga aacaattttg aatcttgctc tcttaaagaa 1818
 agcatcttgt atattaaaaa tcaaaagatg aggctttctt acatatacat cttagttgat 1878
 tatt 1882

<210> 37

<211> 370

<212> PRT

<213> Homo sapiens

<400> 37

Met His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys
 1 5 10 15
 Ser Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala
 20 25 30
 Leu Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp
 35 40 45
 Leu Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val
 50 55 60
 Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
 65 70 75 80
 Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
 85 90 95

158

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
 100 105 110
 Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
 115 120 125
 Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
 130 135 140
 Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
 145 150 155 160
 Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
 165 170 175
 Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
 180 185 190
 Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
 195 200 205
 Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
 210 215 220
 Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
 225 230 235 240
 Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
 245 250 255
 Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
 260 265 270
 Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
 275 280 285
 Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
 290 295 300
 Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
 305 310 315 320
 Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
 325 330 335
 His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
 340 345 350
 Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
 355 360 365
 Pro Arg
 370

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC21.222

159

<400> 38

20

<211> 25

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<223> oligonucleotide primer ZC21,224

25

<211> 25

<213> Artificial Sequence

<223> oligonucleotide primer ZC21,223

25

<211> 21

<213> Artificial Sequence

<223> oligonucleotide primer ZC21,334

21

<211> 3571

<213> Mus musculus

<221> CDS

<222> (1049)...(2086)

<400> 42

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 ctgcccagc acctgttggc ccgccagctg gccgcccgcg cccccgcgc cccccgcgcc 180
 cgcccggccg ccagccccgc gccccgcgcg ccgcccgcctg ggggaaagtg gagacgggga 240
 ggggacaaga gcgacccctc aggccagcca ggccttcctc tagccgcccg tgcttagccg 300
 ccacctctcc tcagccctgc gtctgacctc gccttagggc aggcattccg gcgctcgcga 360
 ctccgagccg cccaagctct cccggcttcc cgcagcactt cgccggtacc cgagggaact 420
 tcggtggcca ccgactgcag caaggaggag gctccgcggt ggatccgggc cagtcccag 480
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 cccaaggtgc tcgcctcgct gccgacctg cttccagtct ggcttggcgg gaccccagat 660
 cctgcctgt gtctgtccc ccaaactgac aggtgctccc tgcgagtcgc cactgactcat 720
 cgccgtctcc ccgctcccc acccttctt tctccctcg cctaccccca cccccgcac 780
 ttggcacag ctccagattt gtttaaacct tgggaaactg gttcaggctc aggttttgct 840
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 attatgtgga aactaccctg cgattctctg ctgccagagc cggccaggcg cttccaccgc 960
 agcgcagcct ttccccggt gggctgagcc ttggagtcgt cgcttcccca gtgcccgcg 1020
 cgagtgcgccc ctgccccag tcagccaa atg ctc ctc ctc ggc ctc ctc ctg 1072

Met Leu Leu Leu Gly Leu Leu Leu

1

5

ctg aca tct gcc ctg gcc ggc caa aga acg ggg act cgg gct gag tcc 1120
 Leu Thr Ser Ala Leu Ala Gly Gln Arg Thr Gly Thr Arg Ala Glu Ser
 10 15 20

aac ctg agc agc aag ttg cag ctc tcc agc gac aag gaa cag aac gga 1168
 Asn Leu Ser Ser Lys Leu Gln Leu Ser Ser Asp Lys Glu Gln Asn Gly
 25 30 35 40

gtg caa gat ccc cgg cat gag aga gtt gtc act ata tct ggt aat ggg 1216
 Val Gln Asp Pro Arg His Glu Arg Val Val Thr Ile Ser Gly Asn Gly
 45 50 55

agc atc cac agc ccg aag ttt cct cat aca tac cca aga aat atg gtg 1264
 Ser Ile His Ser Pro Lys Phe Pro His Thr Tyr Pro Arg Asn Met Val
 60 65 70

ctg gtg tgg aga tta gtt gca gta gat gaa aat gtg cgg atc cag ctg 1312
 Leu Val Trp Arg Leu Val Ala Val Asp Glu Asn Val Arg Ile Gln Leu
 75 80 85

aca ttt gat gag aga ttt ggg ctg gaa gat cca gaa gac gat ata tgc 1360
 Thr Phe Asp Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys
 90 95 100

161

aag tat gat ttt gta gaa gtt gag gag ccc agt gat gga agt gtt tta	1408
Lys Tyr Asp Phe Val Glu Val Glu Glu Pro Ser Asp Gly Ser Val Leu	
105 110 115 120	
gga cgc tgg tgt ggt tct ggg act gtg cca gga aag cag act tct aaa	1456
Gly Arg Trp Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Thr Ser Lys	
125 130 135	
gga aat cat atc agg ata aga ttt gta tct gat gag tat ttt cca tct	1504
Gly Asn His Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser	
140 145 150	
gaa ccc gga ttc tgc atc cac tac agt att atc atg cca caa gtc aca	1552
Glu Pro Gly Phe Cys Ile His Tyr Ser Ile Ile Met Pro Gln Val Thr	
155 160 165	
gaa acc acg agt cct tcg gtg ttg ccc cct tca tct ttg tca ttg gac	1600
Glu Thr Thr Ser Pro Ser Val Leu Pro Pro Ser Ser Leu Ser Leu Asp	
170 175 180	
ctg ctc aac aat gct gtg act gcc ttc agt acc ttg gaa gag ctg att	1648
Leu Leu Asn Asn Ala Val Thr Ala Phe Ser Thr Leu Glu Glu Leu Ile	
185 190 195 200	
cgg tac cta gag cca gat cga tgg cag gtg gac ttg gac agc ctc tac	1696
Arg Tyr Leu Glu Pro Asp Arg Trp Gln Val Asp Leu Asp Ser Leu Tyr	
205 210 215	
aag cca aca tgg cag ctt ttg ggc aag gct ttc ctg tat ggg aaa aaa	1744
Lys Pro Thr Trp Gln Leu Leu Gly Lys Ala Phe Leu Tyr Gly Lys Lys	
220 225 230	
agc aaa gtg gtg aat ctg aat ctc ctc aag gaa gag gta aaa ctc tac	1792
Ser Lys Val Val Asn Leu Asn Leu Leu Lys Glu Glu Val Lys Leu Tyr	
235 240 245	
agc tgc aca ccc cgg aac ttc tca gtg tcc ata cgg gaa gag cta aag	1840
Ser Cys Thr Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys	
250 255 260	
agg aca gat acc ata ttc tgg cca ggt tgt ctc ctg gtc aag cgc tgt	1888
Arg Thr Asp Thr Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys	
265 270 275 280	

acaagcaacc	ttcatcccca	ccagcgttgg	ccgcagggct	ctcagctgct	gatgctggct	2196
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taaatatgga	gccattgcta	acctaccctt	ttctatggga	aataggagta	tagctcagag	3216
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tacacttgta	ttaatacatg	gatattttta	tgtacagaag	tatatcattt	aaggagttca	3396
cttattatac	tctttggcaa	ttgcaaagaa	aatcaacata	atacattgct	tgtaaatgct	3456
taatctgtgc	ccaagttttg	tggtgactat	ttgaattaaa	atgtattgaa	tcatcaaata	3516
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163

<210> 43
 <211> 345
 <212> PRT
 <213> Mus musculus

<400> 43

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Arg	Thr	Gly	Thr	Arg	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Leu	Gln	Leu
			20					25					30		
Ser	Ser	Asp	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Arg	His	Glu	Arg
		35				40					45				
Val	Val	Thr	Ile	Ser	Gly	Asn	Gly	Ser	Ile	His	Ser	Pro	Lys	Phe	Pro
	50				55					60					
His	Thr	Tyr	Pro	Arg	Asn	Met	Val	Leu	Val	Trp	Arg	Leu	Val	Ala	Val
65				70					75					80	
Asp	Glu	Asn	Val	Arg	Ile	Gln	Leu	Thr	Phe	Asp	Glu	Arg	Phe	Gly	Leu
			85					90					95		
Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	Tyr	Asp	Phe	Val	Glu	Val	Glu
		100				105						110			
Glu	Pro	Ser	Asp	Gly	Ser	Val	Leu	Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr
		115				120						125			
Val	Pro	Gly	Lys	Gln	Thr	Ser	Lys	Gly	Asn	His	Ile	Arg	Ile	Arg	Phe
	130					135					140				
Val	Ser	Asp	Glu	Tyr	Phe	Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr
145				150					155					160	
Ser	Ile	Ile	Met	Pro	Gln	Val	Thr	Glu	Thr	Thr	Ser	Pro	Ser	Val	Leu
			165					170					175		
Pro	Pro	Ser	Ser	Leu	Ser	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Val	Thr	Ala
		180				185							190		
Phe	Ser	Thr	Leu	Glu	Glu	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Asp	Arg	Trp
		195				200						205			
Gln	Val	Asp	Leu	Asp	Ser	Leu	Tyr	Lys	Pro	Thr	Trp	Gln	Leu	Leu	Gly
	210				215						220				
Lys	Ala	Phe	Leu	Tyr	Gly	Lys	Lys	Ser	Lys	Val	Val	Asn	Leu	Asn	Leu
225				230						235				240	
Leu	Lys	Glu	Glu	Val	Lys	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	Ser
			245					250					255		
Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	Trp	Pro
		260				265						270			
Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	Cys	Cys	Leu
	275				280							285			
His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Arg	Lys	Val	Thr	Lys	Lys
	290				295						300				

164

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu
 305 310 315 320
 His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
 325 330 335
 Cys Val Cys Arg Gly Asn Ala Gly Gly
 340 345

<210> 44
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC20,572

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 ggcgg 65

<210> 45
 <211> 65
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC20,573

<400> 45
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 tgcac 65

<210> 46
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC19,372

<400> 46
 tgtcgatgaa gccctgaaag acgcgcagac taattcgagc 40

<210> 47
 <211> 60
 <212> DNA

165

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19.351

<400> 47

acgcgcagac taattcgagc tcccaccatc accatcacca cgcgaattcg gtaccgctgg 60

<210> 48

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19.352

<400> 48

actcactata gggcgaattg cccgggggat ccacgcggaa ccagcggtag cgaattcgcg 60

<210> 49

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer ZC19.371

<400> 49

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<210> 50

<211> 1095

<212> DNA

<213> Artificial Sequence

<220>

<223> Fused DNA

<400> 50

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agtaaattcc agttttccag caacaaggaa cagaacggag tacaagatcc tcagcatgag	180
agaattatta ctgtgtctac taatggaagt attcacagcc caaggtttcc tcatacttat	240
ccaagaaata cggctcttgg atggagatta gtagcagtag aggaaaatgt atggatacaa	300
cttacgtttg atgaaagatt tgggcttgaa gaccagaag atgacatatg caagtatgat	360

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66402 "3925450

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